```
# /seqprg/bin/fasta34_t -q -w 80 -m 6 -z 3 -Z 10000 -f -12 -g -4 -r +5/-4 @ /tmp/FA_
FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448
```

Query library @ vs /tmp/FA_WWW_Y37ndo library searching /tmp/FA_WWW_Y37ndo library

```
  1>>>QUERY 1254 nt - 1254 nt
vs  /tmp/FA_WWW_Y37ndo library

   4426 residues in      1 sequences
Altschul/Gish params: n0: 1254 Lambda: 0.192 K: 0.177 H: 0.360

FASTA (3.49 May 2006) function [optimized, +5/-4 matrix (5:-4)] ktup: 6
 join: 60, opt: 45, open/ext: -12/-4, width:  16
Scan time:  0.010
```

```
                                                                  opt bi
The best scores are:
QUERY                                                   (4426) [f] 4546 1
QUERY                                                   (4426) [r]  223 6
```

>>>QUERY, 1254 nt vs /tmp/FA_WWW_Y37ndo library

```
>>QUERY                                                             (4426
 initn: 4881 init1: 3146 opt: 4546  Z-score: 6743.7  bits: 1261.8 E():     0
banded Smith-Waterman score: 4566;  86.321% identity (86.321% similar) in 1272 nt ov
Entrez Lookup  Re-search database  General re-search
                                         10        20        30
QUERY                                    ATGCTCCCCTGGACGGCGCTCGGCCTGGCCCTGAGCT
                                         :::::::::::::::::::::::::::::::::::::::
QUERY  AGCGAGCGAGTTGCCGAGCGCGCCCCGTCCCTCGCGCGCGATGCTCCCCTGGACGGCGCTCGGCCTGGCCCTGAGCT
           20        30        40        50        60        70        80        90

              50        60        70        80        90       100       110
QUERY  GGCTGGCGCTGGCGCGGGAGCGGCGCGGAGCGCGGTCCACCAGCATCAGCCCCCCGAGGGGACCTGATGTTCCTGCTG
       ::::::::::::::::::::::::::::: :::::::::::::::::::::::::::::::::::::::::::::::::::
QUERY  GGCTGGCGCTGGCGCGGGAGCGGCGCGCAGAGCGCGGTCCACCAGCATCAGCCCCCCGAGGGGACCTGATGTTCCTGCTG
          100       110       120       130       140       150       160       170

             130       140       150       160       170       180       190
QUERY  AGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTTCGGGAGTTTGTGGGGCAGCTGGTGGCTCCACTGCCCCT
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QUERY  AGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTTCGGGAGTTTGTGGGGCAGCTGGTGGCTCCACTGCCCCT
          180       190       200       210       220       230       240       250

             210       220       230       240       250       260       270
QUERY  CACCGGGGGCCCTGCGTGCCAGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCCTTCGGCCAGCACAGCT
```

```
                :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QUERY  CACCGGGGCCCTGCGTGCCAGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGCT
       260       270       280       290       300       310       320       330

                    290       300       310       320       330       340       350
QUERY  GTGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCACACTGGCCTGGCGCTGGTCTAT
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QUERY  GTGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCACACTGGCCTGGCGCTGGTCTAT
       340       350       360       370       380       390       400       410

                370       380       390       400       410       420       430
QUERY  AAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGGCCAGGGGTGCCCAAAGTGCTGGTGTGGGTGACAGATGGCGG
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QUERY  AAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGGCCAGGGGTGCCCAAAGTGCTGGTGTGGGTGACAGATGGCGG
       420       430       440       450       460       470       480       490

                450       460       470       480       490       500       510
QUERY  CAGCGACCCTGTGGGCCCCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGAG
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QUERY  CAGCGACCCTGTGGGCCCCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGAG
       500       510       520       530       540       550       560       570

                530       540       550       560       570       580       590
QUERY  ACTTCCTGGAGCTGTCAGCCGCTGCCTCAGCCCCTGCCGAGAAGCACCTGCACTTTGTGGACGTGGATGACCTGCAC
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QUERY  ACTTCCTGGAGCTGTCAGCCGCTGCCTCAGCCCCTGCCGAGAAGCACCTGCACTTTGTGGACGTGGATGACCTGCAC
       580       590       600       610       620       630       640       650

                610       620       630       640       650       660       670
QUERY  ATTGTCCAAGAGCTGAGGGGCTCCATTCT---CGCGATGCGGCCGCAGCAGCTCCATGCCACGGAGATCACGTCCAG
       :::::::::::::::::::::::::::::::   :::::::::::::::::::::::::::::::::::::::::::::::
QUERY  ATTGTCCAAGAGCTGAGGGGCTCCATTCTCGACGCGATGCGGCCGCAGCAGCTCCATGCCACGGAGATCACGTCCAG
       660       670       680       690       700       710       720       730

                680       690       700       710       720       730       740       750
QUERY  CTTCCGCCTGGCCTGGCCACCCCTGCTGACCGCAGACTCGGGCTACTATGTGCTGGAGCTGGTGCCCAGCGCCCAGC
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QUERY  CTTCCGCCTGGCCTGGCCACCCCTGCTGACCGCAGACTCGGGCTACTATGTGCTGGAGCTGGTGCCCAGCGCCCAGC
       740       750       760       770       780       790       800       810

                760       770       780       790       800       810       820       830
QUERY  GGGCTGCAAGACGCCAGCAGCTGCCAGGGAACGCCACGGACTGGATCTGGGCCGGCCTCGACCCGGACACGGACTAC
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QUERY  GGGCTGCAAGACGCCAGCAGCTGCCAGGGAACGCCACGGACTGGATCTGGGCCGGCCTCGACCCGGACACGGACTAC
       820       830       840       850       860       870       880       890

                840       850       860       870       880       890       900       910
QUERY  GTGGCGCTAGTGCCTGAGTCCAACGTGCGCCTCCTGAGGCCCCAGATCCTGCGGGTGCGCACGCGGCCAGAGGAGGC
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::: : ::::
QUERY  GTGGCGCTAGTGCCTGAGTCCAACGTGCGCCTCCTGAGGCCCCAGATCCTGCGGGTGCGCACGCGGCCCGGTGAGGC
       900       910       920       930       940       950       960       970

                920       930       940       950        960       970        98
QUERY  GCCAGAGCGCATCGTCATC----TCCCACGCCCGGCCG-------CGCAGCCTCCGCGTGAGTTGGGCCCCAG----
       ::: : : :: :::        :   ::      ::  :::::      ::::: ::: ::        ::::::::
QUERY  GCC-GGGGGCTTCGGGCCCGGAGTCGGGGGCTGGGCCGGCCCCCACGCAG-CTCGCCGCCCTCCCCGCCCCAGAGGA
       980       990       1000      1010      1020      1030      1040      1050

                990       1000      1010      1020      1030      1040      1050      1
QUERY  TGGGCTCAGCCGCGGCGCTCGGCTACCACGTGCAGTTCGGGCCGCTGCGGGGCGGG--GAGGCGCAGCGGGTGGAGG
```

```
              ::::         :::     :: ::      :: :::::: : :    :: :: ::   : : : : :   : : : :::: : :::
QUERY   CGGGCCAGAGCGCATCG-TCATCTCCCACG-CCCGGCCGCGCAGCCTCCGCGTGAGTTGGGCCCCAGC-GCTGGGCT
        1060        1070        1080        1090        1100        1110        1120        1130

                  1070        1080        1090        1100        1110        1120        1130        1
QUERY   CCGCGGGCCGCAACTGCACCACGCTGCAGGGCCTGGCGCCGGGCACCGCCTACCTGGTGACCGTGACCGCCGCCTTC
        :::::::  : :   ::   ::::::: ::::::   : ::: :    ::          :: : :  :  :   :
QUERY   CCGCGGCGCTCGGCT--ACCACG-TGCAGTTCGGGCCGCTGCGGGGCG------GGGAGGCGCAGCGGGTGGAGGTG
        1140        1150        1160        1170               1180        1190        1200

                  1150        1160        1170        1180        1190        1200        1210
QUERY    TCGGGCCGCGAGAGCGCGCTGTCCGCCAAGGCCTGCACGCCCG--ACGGCCCGCGCCCGCGCCCACGCCCCGTGCCC
         ::::::::: :  ::  :     :   ::  :::::::  ::::  :  :: :::  : :   : : :: :  : ::    :::
QUERY    GCGGGCCGCAACTGCACCACG--CTGCAGGGCCTG-GCGCCGGGCACCGCCTAC-CTGGTGACCGTGACCGCCGCCT
         1210        1220        1230        1240        1250        1260        1270        1

             1220        1230        1240        1250
QUERY    GCCCCGACCCCGGGGACCGCCAGCCGTGAGCCGTAA
         :: : : :: :  : :: ::: :: :: ::  :::
QUERY    GCTCGGGCCGC-GAGAGCGC--GCTGTCCGCCAAGGCCTGCACGCCCGACGGCCCGCGCCCGCGCCCACGCCCCGTG
             1290        1300        1310        1320        1330        1340        1350
```

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```
>>QUERY                                                                        (4426
rev-comp initn: 140 init1:  60 opt: 223  Z-score: 272.1  bits: 64.3  E(): 2.4e-13
banded Smith-Waterman score: 261;  54.659% identity (54.659% similar) in 558 nt over
Entrez Lookup  Re-search database  General re-search
             1240        1230        1220        1210        1200        1190        1180
QUERY-  TCACGGCTGGCGGTCCCCGGGGTCGGGGCGCGGGGCACGGGGCGTGGGCGCGGGCGCGGGC--CGTCG-GGCGTGCA
                                                                       ::: : : : ::: : ::: :   :: :: ::::
QUERY   CCAGCAGCTGCCAGGGAACGCCACGGACTGGATCTGGGCCGGCCTCGACCCGGACACGGACTACGACGTGGCGCTAG
            840         850         860         870         880         890         900         9

           1170        1160        1150        1140        1130        1120        1110        1100
QUERY-  CTTGGCGGACAGCGCG-CTCTCGCGGCCCGAGCGGAAGGCGGCGGTCACGGTCACCAGGTAGGCGGTGCCCGGCGC-
        :: :   :   : ::: ::: : :::::: :::  :    : :: :   ::::   ::  : :::: :::: ::  ::
QUERY   CTGAGTCCAACGTGCGCGCCTCCTGAGGCCCCAGATCCTGCGGGTGCGCACGCGGCCCGGTGAGGCAGGGCCGGGGGCT
           920         930         940         950         960         970         980         9

           1090        1080        1070        1060        1050        1040        1030        1020
QUERY-  GGCCCTGCAGCGTGGTGCAGTTGCGGCCCGCGGGCACCTCCACCCGCTGCGCCTCCCCGCCCCGCAGCGGCCCGAAC
        ::::: : ::   :: :: :  :::::: :  ::: ::    :::  :: :::::::::::::::  :: : ::: :
QUERY   GGCCC-GGAGTCGGGGGGCTGGGCCGGCCCCCACGCAGCT-----CGCCGC-CCTCCCCGCCCCAGAGGAGGCCGGGC
           1000        1010        1020                1030        1040        1050        1060

          1010        1000         990         980         970         960         950         940
QUERY-  ACGTGGTAGCCGAGCGCCGCGGCTGAGCCCA-GCGCTGGGCCCAACTCACGCGGAGGCTGCGCGGCCGGGCGTGGG
        : :::::: :: :     :::: : :   :: :: :    :::: : ::  : :: :  :  :: :::
QUERY   ---------CAGAGCGCATCGTCATCTCCCACGCCCGGCCGCGCAGCCTCCGCGTGAGTTGGGCCCCAGCGC-TGGG
                  1070        1080        1090        1100        1110        1120        11

           930         920         910         900         890         880         870         86
QUERY-  TGACGATGCGCT---CTGGCCCGGCCTCCTCTGGCCGCGTGCGCACCCGCAGGATCTGGGGCCTCAGGAGGCGCACG
        : ::  :::::::   ::  : ::  :   :: :::::: :::: : :  : ::   : ::      ::::: :: ::
QUERY   AGCCGCGGCGCTCGGCTACCACGTGCAGTTCGGGCCGC-TGCGGGGCGG--GGAGGCGCAGCGGGTGGAGGTGCCCG
           1140        1150        1160        1170        1180        1190        1200
```

```
          850         840         830         820         810         800         790
QUERY- GACTCAGGCACTAGCGCCACGTCGTAGTCCGTGTC-CGGGTCGAGGCCGGCC--CAGATCCAGTCCGTGGCGTTCC-
       : : ::    ::: :: :::::  : ::  : :: : : :: :    ::: ::     :: :  : : ::: :: ::::
QUERY  GCCGCA---ACT-GCACCACGCTGCAGGGCCTGGCGCCGGGCACCGCCTACCTGGTGACCGTGACCGCCGCCTTCCG
     1210        1220        1230        1240        1250        1260        1270        1280


          780         770         760         750                 740         730         720
QUERY- TGGCAGCTGCTGGCGTCTTGCAGCCCCCGGCTGGGCGCTGG-------GCACCAGCTCCAGCACATAGTAGCCCGAG
       ::: ::    :     ::  : :::    : :::   ::: :      :: :: :: ::  : :    ::   :::: :
QUERY  GGGCCGCGAGAGCGCGCTGTCCGCCAAGGCCTGCACGCCCGACGGCCCGCGCCCGCGCCCACGCCCCGTGCCCCGCG
           1290        1300        1310        1320        1330        1340        1350        1360


        710         700         690         680         670         660         650         640
QUERY- GCGGTCAGCAGGGGTGGCCAG--GCCAGGCGGAAGCCGCTGGACGTGATCTCCGTGGCATGGAGCTGCTGCGGCCGC
       : : :   :  :::     :::::   :  :: :: ::::::
QUERY  -CCGACCCCGGGGACCGCCAGCCGTGAGCCGTAAGCCGGCGTCCCCGCCCAGCCGAGAGGGCCGGCGCCTACCTGAG
           1370        1380        1390        1400        1410        1420        1430        144
```

```
1254 residues in 1 query    sequences
4426 residues in 1 library sequences
 Tcomplib [34t26] (2 proc)
 start: Thu Sep 28 10:02:00 2006 done: Thu Sep 28 10:02:00 2006
 Total Scan time:  0.010 Total Display time:  0.010

Function used was FASTA [version 3.4t26 July 7, 2006]
```

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